10/521518

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/521,518_

Source: _PU_

Date Processed by STIC: _5/24/06_

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: _10/521,518_   CRF Edit Date: _5/24/06_
                                      Edited by: _Ar_

____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence
text "wrapped" to the next line

____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID
NO's edited:

_____

____ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

____ Inserted mandatory headings/numeric identifiers, specifically:

_____

____ Moved responses to same line as heading/numeric identifier, specifically:

_____

√ Other:
Corrected amino acid numbering in Seqs. 19,21,25
corrected </407, </417 lines

_____

RAW SEQUENCE LISTING   DATE: 05/24/2006
PATENT APPLICATION: US/10/521,518   TIME: 13:48:28

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\05242006\J521518.raw**

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 3 <110> APPLICANT: Expressive Research B.V.
 5 <120> TITLE OF INVENTION: Modulating developmental pathways in plants
 7 <130> FILE REFERENCE: P59845PC00
 9 <140> CURRENT APPLICATION NUMBER: US/10/521,518
 9 <141> CURRENT FILING DATE: 2005-01-18
 9 <150> PRIOR APPLICATION NUMBER: PCT/NL03/00524
10 <151> PRIOR FILING DATE: 2003-07-17
12 <150> PRIOR APPLICATION NUMBER: EP 02077908.8
13 <151> PRIOR FILING DATE: 2002-07-17
15 <160> NUMBER OF SEQ ID NOS: 110
17 <170> SOFTWARE: PatentIn version 3.2
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 227
21 <212> TYPE: PRT
22 <213> ORGANISM: Arabidopsis thaliana
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31             20                  25                  30
34 Cys Gly Cys Cys Leu Leu Ser Leu Phe Val Lys Val Ile Ile Ser Leu
35         35                  40                  45
38 Ile Val Ile Leu Gly Val Ala Ala Leu Ile Phe Trp Leu Ile Val Arg
39     50                  55                  60
42 Pro Arg Ala Ile Lys Phe His Val Thr Asp Ala Ser Leu Thr Arg Phe
43 65                  70                  75                  80
46 Asp His Thr Ser Pro Asp Asn Ile Leu Arg Tyr Asn Leu Ala Leu Thr
47                 85                  90                  95
50 Val Pro Val Arg Asn Pro Asn Lys Arg Ile Gly Leu Tyr Tyr Asp Arg
51             100                 105                 110
54 Ile Glu Ala His Ala Tyr Tyr Glu Gly Lys Arg Phe Ser Thr Ile Thr
55         115                 120                 125
58 Leu Thr Pro Phe Tyr Gln Gly His Lys Asn Thr Thr Val Leu Thr Pro
59     130                 135                 140
62 Thr Phe Gln Gly Gln Asn Leu Val Ile Phe Asn Ala Gly Gln Ser Arg
63 145                 150                 155                 160
66 Thr Leu Asn Ala Glu Arg Ile Ser Gly Val Tyr Asn Ile Glu Ile Lys
67                 165                 170                 175
70 Phe Arg Leu Arg Val Arg Phe Lys Leu Gly Asp Leu Lys Phe Arg Arg
71             180                 185                 190
74 Ile Lys Pro Lys Val Asp Cys Asp Asp Leu Arg Leu Pro Leu Ser Thr
75             195                 200                 205
78 Ser Asn Gly Thr Thr Thr Thr Ser Thr Val Phe Pro Ile Lys Cys Asp
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82 Phe Asp Phe
83 225
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87 <211> LENGTH: 416
88 <212> TYPE: PRT
89 <213> ORGANISM: Arabidopsis thaliana
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97 Thr His Phe Asp Leu Glu Ser Asn Asn Asn Leu Gln Tyr Ser Leu Ser
98              20                  25                  30
101 Leu Asn Leu Ser Ile Arg Asn Ser Lys Ser Ser Ile Gly Ile His Tyr
102             35                  40                  45
105 Asp Arg Phe Glu Ala Thr Val Tyr Tyr Met Asn Gln Arg Leu Gly Ala
106     50                  55                  60
109 Val Pro Met Pro Leu Phe Tyr Leu Gly Ser Lys Asn Thr Met Leu Leu
110 65                  70                  75                  80
113 Arg Ala Leu Phe Glu Gly Gln Thr Leu Val Leu Leu Lys Gly Asn Glu
114             85                  90                  95
117 Arg Lys Lys Phe Glu Asp Asp Gln Lys Thr Gly Val Tyr Arg Ile Asp
118             100                 105                 110
121 Val Lys Leu Ser Ile Asn Phe Arg Val Met Val Leu His Leu Val Thr
122             115                 120                 125
125 Trp Pro Met Lys Pro Val Val Arg Cys His Leu Lys Ile Pro Leu Ala
126     130                 135                 140
129 Leu Gly Ser Ser Asn Ser Thr Gly Gly His Lys Lys Met Leu Leu Ile
130 145                 150                 155                 160
133 Gly Gln Leu Val Lys Asp Thr Ser Ala Asn Leu Arg Glu Ala Ser Glu
134             165                 170                 175
137 Thr Asp His Arg Arg Asp Val Ala Gln Ser Lys Lys Ile Ala Asp Ala
138             180                 185                 190
141 Lys Leu Ala Lys Asp Phe Glu Ala Ala Leu Lys Glu Phe Gln Lys Ala
142     195                 200                 205
145 Gln His Ile Thr Val Glu Arg Glu Thr Ser Tyr Ile Pro Phe Asp Pro
146     210                 215                 220
149 Lys Gly Ser Phe Ser Ser Ser Glu Val Asp Ile Gly Tyr Asp Arg Ser
150 225                 230                 235                 240
153 Gln Glu Gln Arg Val Leu Met Glu Ser Arg Arg Gln Glu Ile Val Leu
154             245                 250                 255
157 Leu Asp Asn Glu Ile Ser Leu Asn Glu Ala Arg Ile Glu Ala Arg Glu
158             260                 265                 270
161 Gln Gly Ile Gln Glu Val Lys His Gln Ile Ser Glu Val Met Glu Met
162     275                 280                 285
165 Phe Lys Asp Leu Ala Val Met Val Asp His Gln Gly Thr Ile Asp Asp
166     290                 295                 300
169 Ile Asp Glu Lys Ile Asp Asn Leu Arg Ser Ala Ala Ala Gln Gly Lys
170 305                 310                 315                 320
173 Ser His Leu Val Lys Ala Ser Asn Thr Gln Gly Ser Asn Ser Ser Leu
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              RAW SEQUENCE LISTING              DATE: 05/24/2006
              PATENT APPLICATION:  US/10/521,518    TIME: 13:48:28

              Input Set : A:\PTO.AMC.txt
              Output Set: N:\CRF4\05242006\J521518.raw

174                 325                330                335
177 Leu Phe Ser Cys Ser Leu Leu Leu Phe Phe Phe Leu Ser Gly Asp Leu
178             340                345                350
181 Cys Arg Cys Val Cys Val Gly Ser Glu Asn Pro Arg Leu Asn Pro Thr
182         355                360                365
185 Arg Arg Lys Ala Trp Cys Glu Glu Glu Asp Glu Glu Gln Arg Lys Lys
186     370                375                380
189 Gln Gln Lys Lys Lys Thr Met Ser Glu Lys Arg Arg Arg Glu Glu Lys
190 385                390                395                400
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194             405                410                415
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198 <211> LENGTH: 1634
199 <212> TYPE: DNA
200 <213> ORGANISM: Arabidopsis thaliana
203 <220> FEATURE:
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205 <222> LOCATION: (501)..(563)
206 <223> OTHER INFORMATION: signal sequence (exon 1)
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209 <221> NAME/KEY: CDS
210 <222> LOCATION: (655)..(708)
211 <223> OTHER INFORMATION: propeptide (exon 2)
213 <220> FEATURE:
214 <221> NAME/KEY: CDS
215 <222> LOCATION: (797)..(856)
216 <223> OTHER INFORMATION: propeptide (exon 3)
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219 <221> NAME/KEY: CDS
220 <222> LOCATION: (955)..(1131)
221 <223> OTHER INFORMATION: conserved cysteine motif (exon 4)
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226 ctatctctct cagtgtcaca atgtctgaac taagagacag ctgtaaacta tcattaagac   120
228 ataaactacc aaagtatcaa gctaatgtaa aaattactct catttccacg taacaaattg   180
230 agttagctta agatattagt gaaactaggt ttgaattttc ttcttcttct tccatgcatc   240
232 ctccgaaaaa agggaaccaa tcaaaactgt ttgcatatca aactccaaca ctttacagca   300
234 aatgcaatct ataatctgtg atttatccaa taaaaacctg tgatttatgt ttggctccag   360
236 cgatgaaagt ctatgcatgt gatctctatc caacatgagt aattgttcag aaaataaaaa   420
238 gtagctgaaa tgtatctata taaagaatca tccacaagta ctattttcac acactacttc   480
240 aaaatcacta ctcaagaaat atg aag aag atg aat gtg gtg gct ttt gtt acg   533
241                         Met Lys Lys Met Asn Val Val Ala Phe Val Thr
242                          1           5                   10
244 ctg atc atc tct ttt ctt ctg ctt tct cag gtaaactgtt aaaaccattt       583
245 Leu Ile Ile Ser Phe Leu Leu Leu Ser Gln
246         15                  20
248 tcaagactac cttttctcta tttcagacaa accaaagtaa aacaatgaaa aatctctctg   643
250 gtctttcata g gta ctt gca gag ttg tca tca tcc agc aac aat gaa act    693
251           Val Leu Ala Glu Leu Ser Ser Ser Ser Asn Asn Glu Thr
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252                         25                    30
254 tcc tct gtt tct cag gtaagagtga tacaaaaaca tactaaacaa actttcaaga      748
255 Ser Ser Val Ser Gln
256 35
258 gagtaatata taaggaaatg ttggcttctt tttttgttg ctaatcag acg aat gac      805
259                                                          Thr Asn Asp
260                                                              40
262 gag aac caa act gcg gcg ttt aag aga aca tac cac cat cgt cca aga      853
263 Glu Asn Gln Thr Ala Ala Phe Lys Arg Thr Tyr His His Arg Pro Arg
264        45                  50                  55
266 atc agttagtcta ctctttcaac actctaattc ctttgttcta agtattttt           906
267 Ile
270 ttgccccca caacctttt tttattaaat gagccaattt ttatagat tgt ggg cat       963
271                                                        Cys Gly His
272                                                            60
274 gca tgc gca agg aga tgc agt aag aca tcg agg aag aaa gtt tgt cac     1011
275 Ala Cys Ala Arg Arg Cys Ser Lys Thr Ser Arg Lys Lys Val Cys His
276        65                  70                  75
278 aga gcc tgt gga agt tgt tgt gcc aag tgt cag tgt gtg ccg ccg gga     1059
279 Arg Ala Cys Gly Ser Cys Cys Ala Lys Cys Gln Cys Val Pro Pro Gly
280    80                  85                  90
282 acc tcc ggc aac aca gca tca tgt cct tgc tac gcc agt atc cgt aca     1107
283 Thr Ser Gly Asn Thr Ala Ser Cys Pro Cys Tyr Ala Ser Ile Arg Thr
284 95                  100                 105                 110
286 cat ggc aat aaa ctc aaa tgt cct taaaagactt ctcattctc aactatagtc    1161
287 His Gly Asn Lys Leu Lys Cys Pro
288                     115
290 tcatcttctg attatgtttc ttcttttgtt atgttgcatg tgtgatgtgt gagcttatta  1221
292 ttatgttgat tgttgacata attcaactat ataatttgta tcgattccga ataataagat  1281
294 gagtgatttt attggctatt aagttttttt ttttttttt tgggcacaat ggctattaag   1341
296 ttttaaacat ctgatttat tggttacaaa aaacaacaaa gtttcatttt catattaaca    1401
298 caaaatctcc atacatatta ccaaaccaaa aaaatacaca aggggagag agaccaacgg    1461
300 ttcttggttc agagtttgca tcttgtttga ccgtcaccg tttcttagac ttaacagcca    1521
302 caacacctttt ataaagcttc acgcgatcct tcaacgcatc tcgccgaggc cgagccacct  1581
304 tattgtttgg atcaaacaac aaaacttctt caaacgcatt caatgccaaa ggc          1634
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307 <210> SEQ ID NO: 4
308 <211> LENGTH: 118
309 <212> TYPE: PRT
310 <213> ORGANISM: Arabidopsis thaliana
312 <400> SEQUENCE: 4

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318 Leu Leu Leu Ser Gln Val Leu Ala Glu Leu Ser Ser Ser Ser Asn Asn
319             20                  25                  30
322 Glu Thr Ser Ser Val Ser Gln Thr Asn Asp Glu Asn Gln Thr Ala Ala
323             35                  40                  45
326 Phe Lys Arg Thr Tyr His His Arg Pro Arg Ile Cys Gly His Ala Cys
327     50                  55                  60
330 Ala Arg Arg Cys Ser Lys Thr Ser Arg Lys Lys Val Cys His Arg Ala
```

```
331 65                   70                   75                   80
334 Cys Gly Ser Cys Cys Ala Lys Cys Gln Cys Val Pro Pro Gly Thr Ser
335                   85                   90                   95
338 Gly Asn Thr Ala Ser Cys Pro Cys Tyr Ala Ser Ile Arg Thr His Gly
339              100                 105                 110
342 Asn Lys Leu Lys Cys Pro
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347 <211> LENGTH: 1453
348 <212> TYPE: DNA
349 <213> ORGANISM: Arabidopsis thaliana
352 <220> FEATURE:
353 <221> NAME/KEY: CDS
354 <222> LOCATION: (501)..(533)
355 <223> OTHER INFORMATION: signal peptide (exon 1)
357 <220> FEATURE:
358 <221> NAME/KEY: CDS
359 <222> LOCATION: (664)..(691)
360 <223> OTHER INFORMATION: propeptide (exon 2)
362 <220> FEATURE:
363 <221> NAME/KEY: CDS
364 <222> LOCATION: (772)..(950)
365 <223> OTHER INFORMATION: conserved cysteine motif (exon 3)
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368 gaaaaaaga agaaaagata atggtccgta ttaatatagt tgaaaacttg aaactacttt      60
370 ttagtttgta tataatacag tagactaggg atccagttga gtttctttct ttattttgag     120
372 tttgtgttta tgtttgattt tacgttttta tatgtaaata agatatttta cgaattatgg     180
374 ttttatttgg gtagaagttg tagaatgact taaacaatca agtggcagaa tgagatatat     240
376 aaagtaatat aatatatgta ccgttattaa cttattgtac atgtgaatga ggaagcttac     300
378 acacacacac cttctataaa tagctgacaa aactggttgt tacacacaac acattcataa     360
380 atctctcaaa gtaagaacta agagctttac tacagtccta ctctctacac atcttctctc     420
382 tctctcaaga gctagtcatg gccaaactca taacttcttt tctcttactc acaattttat     480
384 tcactttcgt ttgtctcact atg tca aaa gaa gct gag tac cat cca gaa agt     533
385                         Met Ser Lys Glu Ala Glu Tyr His Pro Glu Ser
386                         1               5                   10
388 gtaagttttt attttttggt aaaatagaaa gtgtaagttt tataattcat tcaattgttt     593
390 ttgcctttcc ctttctattt attgctataa atctaatacc cgcgttaaaa tttgttttga     653
392 aattaaacag tat gga cca gga agt ctg aaa tca tac c gtaagtaaaa           701
393             Tyr Gly Pro Gly Ser Leu Lys Ser Tyr
394                         15                  20
396 acttcttctt cttttatgaa tcttgtttct tattatatat caaataaaaa ctcgattatc     761
398 atgattgcag aa  tgt gga gga caa tgc aca agg aga tgt agc aac aca        809
399             Gln Cys Gly Gly Gln Cys Thr Arg Arg Cys Ser Asn Thr
400                         25                  30
402 aag tat cat aag cca tgc atg ttc ttc tgc caa aag tgt tgt gct aaa      857
403 Lys Tyr His Lys Pro Cys Met Phe Phe Cys Gln Lys Cys Cys Ala Lys
404     35                  40                  45
406 tgc ctt tgt gtc cct cca ggc acg tac ggc aac aaa caa gtg tgt cct      905
407 Cys Leu Cys Val Pro Pro Gly Thr Tyr Gly Asn Lys Gln Val Cys Pro
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/24/2006
PATENT APPLICATION: US/10/521,518   TIME: 13:48:29

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\05242006\J521518.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:31; Xaa Pos. 2,4,7,8,9,10,11,12,13,14,16,17,18,20,21,24,25,27,31,34,36
Seq#:31; Xaa Pos. 37,38,39,41,44,45,46,47,48,49,50,52,53

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:25; Line(s) 1786

VERIFICATION SUMMARY   DATE: 05/24/2006
PATENT APPLICATION: **US/10/521,518**   TIME: 13:48:29

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF4\05242006\J521518.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:517 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 7
L:1047 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 15
L:1311 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19
L:2187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31 after pos.:0
M:341 Repeated in SeqNo=31